SEQUENCE LISTING

<110> Vaisvila, Romualdus
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Claus, Toby B.
Raleigh, Elisabeth A.

<120> Method For Cloning And Producing The MseI Restriction Endonuclease

<130> NEB-181

<140> US 09/689,343
<141> 2000-10-12

<160> 9

<170> PatentIn version 3.1

<210> 1
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<212> DNA
<213> Micrococcus sp.

<220>
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Met Pro Ile Ser Thr Val Trp Thr Pro Asp Gly Asp Asp Leu Ile Val
1               5                  10                  15

gag gcg gac aac ctc gat ttc att caa acg ctc ccc gac gcg agc ttc       96
Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
            20                  25                  30

cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag cgg      144
Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
        35                  40                  45

ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc      192
Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
    50                  55                  60

ttc aaa ggc cag acg tac gac acg gtc aag agc act ctg cac tcg tat      240
Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
65                  70                  75                  80

gac gac gct ttc acc gac tat tgg tcg ttc ctc gaa ccg cgt ctc ctg      288
Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
                85                  90                  95
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gag gct tgg cgg ttg ctc acc cct gac ggc gcg ctc tat ctt cat ctg      336
Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
            100                 105                 110

gat tac cgc gag gtt cac tac gcc aag gtc gtc ctc gac gcg atg ttc      384
Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
        115                 120                 125

gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc      432
Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
    130                 135                 140

gcg cgc tcg aag agc aag tgg ccc acc aag cac gac aac atc ctc gtg      480
Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
145                 150                 155                 160

tat gtg aag gac ccg aac aac tac gtc tgg aac ggt cag gat gta gat      528
Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
                165                 170                 175

cgc gag ccc tac atg gcg ccc ggg ctc gtt aca ccc gag aag gta gcg      576
Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
            180                 185                 190

ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct      624
Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
        195                 200                 205

gcg agc aaa gag cgc acc ggg tac gcg aca cag aag ccg gtc ggc atc      672
Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
    210                 215                 220

atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg      720
Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
225                 230                 235                 240

gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcg gcc cgc cag ctc      768
Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
                245                 250                 255

gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta      816
Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
            260                 265                 270

atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc      864
Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
        275                 280                 285

gtg cag act ccc cag agt gac cca cga acc gac gga tga                  903
Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
    290                 295                 300
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<212> PRT
<213> Micrococcus sp.

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20 25 30

Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
35 40 45

Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
50 55 60

Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
65 70 75 80

Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
85 90 95

Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
100 105 110

Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
115 120 125

Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
130 135 140

Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
145 150 155 160

Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
165 170 175

Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
180 185 190

Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
195 200 205

Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
210 215 220

Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
225 230 235 240

Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
245 250 255

Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
260 265 270

Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
275 280 285

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Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
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<213> Unknown

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<221> misc_feature
<222> (198)..(198)
<223> Xaa = any amino acid

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<222> (594)..(594)
<223> N= G, A, C or T

<400> 3

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Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala
1               5                   10                  15

acc tcc ttg cat ctg gag agt gtg gtc act gag gga gcg gag tca ccg       96
Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
            20                  25                  30

cct aat cgt ctg att tgg gcg gac aac ctg ccg cta atg gta gat ttg      144
Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
        35                  40                  45

ttg gcc gaa tat gaa ggg aaa atc gat ctg atc tac gcc gat ccc cct      192
Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
    50                  55                  60

ttt ttt acg gat cgt act tat gcg gcg cga att ggt cat ggg gag gat      240
Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
65                  70                  75                  80

tcg cgt cgt cca caa acc tgg cag ctt gca gaa gga tat acg gac gag      288
Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
                85                  90                  95

tgg aag gat tta gat gaa tac ctg gac ttc ctt tat cca cgc ctg gta      336
Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
            100                 105                 110
```

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ctg atg tat cga ctg ctg gca cca cac gga acg ctc tac ttg cac ctg      384
Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
        115                 120                 125

gac tgg cac gcc aat gcc tac gta cgt gta ctg ctt gat gag atc ttc      432
Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
    130                 135                 140

ggg cga cag cgg ttt ctc aac gag atc gtc tgg atc tat cac ggc ccc      480
Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
145                 150                 155                 160

tca gcc atc cga cgc gcc ttc aag cgc aaa cat gat acc atc ttg gtt      528
Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
                165                 170                 175

tat gtg aaa ggt gaa aac tat aca ttc aat gcg gat gcg gtt cgt caa      576
Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
            180                 185                 190

cct tac cat ccg agc acn cat aag acc ttc gct tcc tcc ccg aag gcc      624
Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
        195                 200                 205

ggc ttt ggt aag gtg ccg gat ctg cag cgc ggc aaa gtg ccc gaa gac      672
Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
    210                 215                 220

tgg tgg tat ttt ccg gtc gtg gcc cgt cta cac cga gaa cgg agc ggc      720
Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly
225                 230                 235                 240

tat ccg act caa aag cct caa gcc ttg ctg gag cgg atc ctg ctg gcc      768
Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala
                245                 250                 255

tcc tcg aac gca ggc gat ctg gtg gca gac ttc ttc tgc ggc tca ggg      816
Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly
            260                 265                 270

aca acc gct gtg gtg gca gcc cgt ctg gga cgg cgc ttc ctg gtc aac      864
Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn
        275                 280                 285

gat gca agc tgg cgc gcc gtt cat gtg aca cgc aca cgc ttg cta cgc      912
Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg
    290                 295                 300

gag gga gta agt ttc act ttt gaa cgc cag gaa act ttt act cta cct      960
Glu Gly Val Ser Phe Thr Phe Glu Arg Gln Glu Thr Phe Thr Leu Pro
305                 310                 315                 320

atc cag cca ctt cca cca gat tgg ttg atc atc gcc gag gag cag att     1008
Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile
                325                 330                 335
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cgc ctc caa gca ccc ttt ctc gta gat ttt tgg gaa gtg gac gat caa     1056
Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln
            340                 345                 350

tgg gat ggc aaa atc ttc cgc agc cgt cat caa ggc tta cgc tcc cgc     1104
Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg
        355                 360                 365

ctt cag gag cag gcg ccg ctc tct cta cca ttg acc ggg aat gga ctg     1152
Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
    370                 375                 380

ttg tgt gta cgg gta gtg agc cgt gaa ggg gaa tac tat gag ttc aca     1200
Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr
385                 390                 395                 400

ggt cga gcc gat agc cct cac ccc gta tcg ttt tga                     1236
Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
                405                 410
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<210> 4
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<213> Unknown

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<222> (198)..(198)
<223> Xaa = any amino acid

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Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
            20                  25                  30

Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
        35                  40                  45

Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
    50                  55                  60

Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
65                  70                  75                  80

Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
                85                  90                  95

Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
            100                 105                 110
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```
Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
        115                 120                 125

Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
    130                 135                 140

Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
145                 150                 155                 160

Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
                165                 170                 175

Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
            180                 185                 190

Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
        195                 200                 205

Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
    210                 215                 220

Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly
225                 230                 235                 240

Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala
                245                 250                 255

Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly
            260                 265                 270

Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn
        275                 280                 285

Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg
    290                 295                 300

Glu Gly Val Ser Phe Thr Phe Glu Arg Gln Glu Thr Phe Thr Leu Pro
305                 310                 315                 320

Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile
                325                 330                 335

Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln
            340                 345                 350

Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg
        355                 360                 365

Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
    370                 375                 380

Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr
385                 390                 395                 400

Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
                405                 410
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<211> 924
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<220>
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<220>
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<223>

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1               5                  10                  15

gcc gac aac atg gaa gtc ctg cga ggg ctt ccg gcg gcg tcc gtg gac       96
Ala Asp Asn Met Glu Val Leu Arg Gly Leu Pro Ala Ala Ser Val Asp
            20                  25                  30

ctg atc tac atc gat cct ccg ttc aac acc gga aag gtt cag gag cgc      144
Leu Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Lys Val Gln Glu Arg
        35                  40                  45

act cag ctc aaa acg gtg cgc tcc gag tgg ggc gat cgc gtc gga ttc      192
Thr Gln Leu Lys Thr Val Arg Ser Glu Trp Gly Asp Arg Val Gly Phe
    50                  55                  60

cag ggc cgt cgc tac gaa agc atc gtc gtg ggt aag aag cgc ttt acc      240
Gln Gly Arg Arg Tyr Glu Ser Ile Val Val Gly Lys Lys Arg Phe Thr
65                  70                  75                  80

gac ttc ttc gac gac tat ctg gct ttc ctg gaa ccg cgc ctg gtc gaa      288
Asp Phe Phe Asp Asp Tyr Leu Ala Phe Leu Glu Pro Arg Leu Val Glu
                85                  90                  95

gcc cat cgt gtt ctg gcg ccg cac ggg tgc ctc tac ttt cac gtc gac      336
Ala His Arg Val Leu Ala Pro His Gly Cys Leu Tyr Phe His Val Asp
            100                 105                 110

tac cgc gag gtg cac tac tgt aag gtc ctt ctt gac ggc atc ttc ggt      384
Tyr Arg Glu Val His Tyr Cys Lys Val Leu Leu Asp Gly Ile Phe Gly
        115                 120                 125

cgc gag gcc ttt ctc aac gag atc atc tgg gcc tac gat tac ggc ggg      432
Arg Glu Ala Phe Leu Asn Glu Ile Ile Trp Ala Tyr Asp Tyr Gly Gly
    130                 135                 140

cgt ccg aag gac agg tgg cct cct aag cac gac aac atc ctg ctc tac      480
Arg Pro Lys Asp Arg Trp Pro Pro Lys His Asp Asn Ile Leu Leu Tyr
145                 150                 155                 160
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gcc aag act ccc ggt cgc cac gtg ttc aat gcg gac gaa atc gag cgc      528
Ala Lys Thr Pro Gly Arg His Val Phe Asn Ala Asp Glu Ile Glu Arg
                165                 170                 175

att ccc tac atg gct ccg ggc ctg gtt ggc ccc gaa aag gca gcc cgt      576
Ile Pro Tyr Met Ala Pro Gly Leu Val Gly Pro Glu Lys Ala Ala Arg
            180                 185                 190

gga aaa ctg cca acc gac acg tgg tgg cat acg atc gtt ccg acc agc      624
Gly Lys Leu Pro Thr Asp Thr Trp Trp His Thr Ile Val Pro Thr Ser
        195                 200                 205

ggc tcc gag aag acc ggg tat cca acc cag aaa cct tta ggg att ctc      672
Gly Ser Glu Lys Thr Gly Tyr Pro Thr Gln Lys Pro Leu Gly Ile Leu
    210                 215                 220

cgc cgt att gtg cag gca tcg tct cat ccg ggg gca gtc gtg ctc gac      720
Arg Arg Ile Val Gln Ala Ser Ser His Pro Gly Ala Val Val Leu Asp
225                 230                 235                 240

ttc ttc gcc ggc agt ggg aca aca ggg gta gcg gct ttt gag ttg ggc      768
Phe Phe Ala Gly Ser Gly Thr Thr Gly Val Ala Ala Phe Glu Leu Gly
                245                 250                 255

cgg cgt ttc att ctg gtc gat aac cat ccg gag gcc ctc cag gtg atg      816
Arg Arg Phe Ile Leu Val Asp Asn His Pro Glu Ala Leu Gln Val Met
            260                 265                 270

gcc agg cgc ttc gac ggc atc gag ggg atc gaa tgg gtg ggc ttc gat      864
Ala Arg Arg Phe Asp Gly Ile Glu Gly Ile Glu Trp Val Gly Phe Asp
        275                 280                 285

ccg aca ccg tac cag aag ggc gca aag cag cgc cgc tcc tgc ccg gcg      912
Pro Thr Pro Tyr Gln Lys Gly Ala Lys Gln Arg Arg Ser Cys Pro Ala
    290                 295                 300

ccc acc ggg taa                                                    924
Pro Thr Gly
305
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<220>
<223> Environmental DNA

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Ala Asp Asn Met Glu Val Leu Arg Gly Leu Pro Ala Ala Ser Val Asp
            20                  25                  30
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Leu Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Lys Val Gln Glu Arg
        35                  40                  45

Thr Gln Leu Lys Thr Val Arg Ser Glu Trp Gly Asp Arg Val Gly Phe
    50                  55                  60

Gln Gly Arg Arg Tyr Glu Ser Ile Val Val Gly Lys Lys Arg Phe Thr
65                  70                  75                  80

Asp Phe Phe Asp Asp Tyr Leu Ala Phe Leu Glu Pro Arg Leu Val Glu
                85                  90                  95

Ala His Arg Val Leu Ala Pro His Gly Cys Leu Tyr Phe His Val Asp
            100                 105                 110

Tyr Arg Glu Val His Tyr Cys Lys Val Leu Leu Asp Gly Ile Phe Gly
        115                 120                 125

Arg Glu Ala Phe Leu Asn Glu Ile Ile Trp Ala Tyr Asp Tyr Gly Gly
    130                 135                 140

Arg Pro Lys Asp Arg Trp Pro Pro Lys His Asp Asn Ile Leu Leu Tyr
145                 150                 155                 160

Ala Lys Thr Pro Gly Arg His Val Phe Asn Ala Asp Glu Ile Glu Arg
                165                 170                 175

Ile Pro Tyr Met Ala Pro Gly Leu Val Gly Pro Glu Lys Ala Ala Arg
            180                 185                 190

Gly Lys Leu Pro Thr Asp Thr Trp Trp His Thr Ile Val Pro Thr Ser
        195                 200                 205

Gly Ser Glu Lys Thr Gly Tyr Pro Thr Gln Lys Pro Leu Gly Ile Leu
    210                 215                 220

Arg Arg Ile Val Gln Ala Ser Ser His Pro Gly Ala Val Val Leu Asp
225                 230                 235                 240

Phe Phe Ala Gly Ser Gly Thr Thr Gly Val Ala Ala Phe Glu Leu Gly
                245                 250                 255

Arg Arg Phe Ile Leu Val Asp Asn His Pro Glu Ala Leu Gln Val Met
            260                 265                 270

Ala Arg Arg Phe Asp Gly Ile Glu Gly Ile Glu Trp Val Gly Phe Asp
        275                 280                 285

Pro Thr Pro Tyr Gln Lys Gly Ala Lys Gln Arg Arg Ser Cys Pro Ala
    290                 295                 300

Pro Thr Gly
305
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<213> Micrococcus sp.

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<223>

<400> 7

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Val Thr His Glu Pro Thr Asp Asp Pro Asp Phe Ile Val Met Ala Ala
1               5                  10                  15

agc gcg gcg aac ctc gct gat cgg tac gta gcg agt gaa gac gac ccc       96
Ser Ala Ala Asn Leu Ala Asp Arg Tyr Val Ala Ser Glu Asp Asp Pro
            20                  25                  30

tgg gtc ggc agc ccg ttc gag tgg atc ctt cgc gtt cca tcc aga acg      144
Trp Val Gly Ser Pro Phe Glu Trp Ile Leu Arg Val Pro Ser Arg Thr
        35                  40                  45

aag ggc gcg gtc ggt gag ctg ctc gtg agc gaa tgg gct aat gcc aaa      192
Lys Gly Ala Val Gly Glu Leu Leu Val Ser Glu Trp Ala Asn Ala Lys
    50                  55                  60

ggc ctc cgt gtg aag agg tcg ggg tcc agc gat gcg gac cgc gtg atc      240
Gly Leu Arg Val Lys Arg Ser Gly Ser Ser Asp Ala Asp Arg Val Ile
65                  70                  75                  80

aac ggg cat cgc atc gag atc aag atg tcg act ttg tgg aag tcc ggc      288
Asn Gly His Arg Ile Glu Ile Lys Met Ser Thr Leu Trp Lys Ser Gly
                85                  90                  95

ggc ttc aag ttt cag cag atc cgg gat cag gag tac gac ttt tgc ctc      336
Gly Phe Lys Phe Gln Gln Ile Arg Asp Gln Glu Tyr Asp Phe Cys Leu
            100                 105                 110

tgc ctt ggg atc agc ccg ttc gaa gtg cac gcg tgg ctg ctg ccc aaa      384
Cys Leu Gly Ile Ser Pro Phe Glu Val His Ala Trp Leu Leu Pro Lys
        115                 120                 125

gac cta ttg ctt gag tac gtg att ggt cac atg ggt cag cac acc ggc      432
Asp Leu Leu Leu Glu Tyr Val Ile Gly His Met Gly Gln His Thr Gly
    130                 135                 140

gcg agc ggg agc gac act gcg tgg ctg ggg ttc cca gcg gac gag ccg      480
Ala Ser Gly Ser Asp Thr Ala Trp Leu Gly Phe Pro Ala Asp Glu Pro
145                 150                 155                 160

tat gac tgg atg cgc cct ttc gga ggt cgc tta ggt cac gtc gaa gat      528
Tyr Asp Trp Met Arg Pro Phe Gly Gly Arg Leu Gly His Val Glu Asp
                165                 170                 175
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ctc ctc ctc gcg gcc ggc ccc ggt ccc tac tga 561
Leu Leu Leu Ala Ala Gly Pro Gly Pro Tyr
180 185

<210> 8
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<212> PRT
<213> Micrococcus sp.

<400> 8

Val Thr His Glu Pro Thr Asp Asp Pro Asp Phe Ile Val Met Ala Ala
1 5 10 15

Ser Ala Ala Asn Leu Ala Asp Arg Tyr Val Ala Ser Glu Asp Asp Pro
20 25 30

Trp Val Gly Ser Pro Phe Glu Trp Ile Leu Arg Val Pro Ser Arg Thr
35 40 45

Lys Gly Ala Val Gly Glu Leu Leu Val Ser Glu Trp Ala Asn Ala Lys
50 55 60

Gly Leu Arg Val Lys Arg Ser Gly Ser Ser Asp Ala Asp Arg Val Ile
65 70 75 80

Asn Gly His Arg Ile Glu Ile Lys Met Ser Thr Leu Trp Lys Ser Gly
85 90 95

Gly Phe Lys Phe Gln Gln Ile Arg Asp Gln Glu Tyr Asp Phe Cys Leu
100 105 110

Cys Leu Gly Ile Ser Pro Phe Glu Val His Ala Trp Leu Leu Pro Lys
115 120 125

Asp Leu Leu Leu Glu Tyr Val Ile Gly His Met Gly Gln His Thr Gly
130 135 140

Ala Ser Gly Ser Asp Thr Ala Trp Leu Gly Phe Pro Ala Asp Glu Pro
145 150 155 160

Tyr Asp Trp Met Arg Pro Phe Gly Gly Arg Leu Gly His Val Glu Asp
165 170 175

Leu Leu Leu Ala Ala Gly Pro Gly Pro Tyr
180 185

<210> 9
<211> 413
<212> DNA
<213> Escherichia coli

<400> 9

accggtgatt ggacattgcc gaaatcaggc tgtctctcac tatttgacgc actggctgga 60

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ccggtttttt ttgcgttgaa tttgtcattt tgtgccgtgg tgtttaaacc gcacagaata 180

aattgtcgtg atttcacctt taaaataaaa ttaaaagaga aaaaaattct ctgtggaagg 240

gctatgttag ataaaattga ccgtaagctg ctggccttac tgcagcagga ttgcaccctc 300

tctttgcagg cactggctga agccgttaat ctgacaacca ccccttgctg gaagcgcctg 360

aaacggctgg aggacgacgg tatccttatc ggcaaagtcg ccctgctgga tcc 413

Dl
core